Figure 1

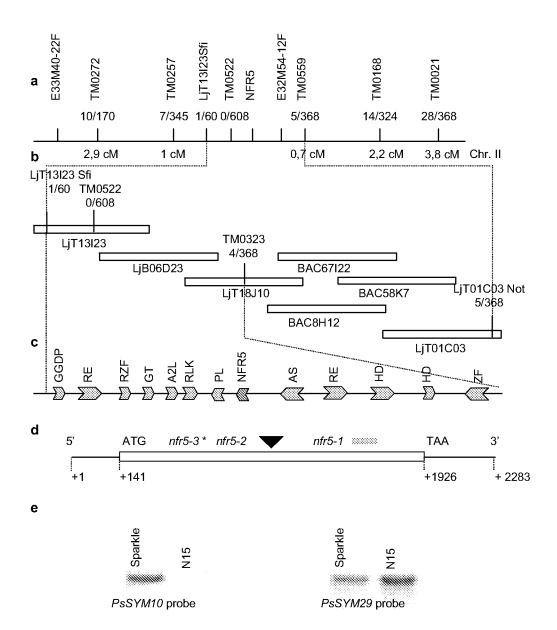


Figure 2

a

SP LysM1 LysM2 LysM3 TM Kinase	
b	
MAVFFLTSGSLSLFLALTLLFTNIAA	SP
RSEKISGPDFSCPVDSPPSCETYVT	51 aa
Y TAQSPNLLSLTNISDIFDISPLSIARAS N IDAGKDKLVPGQ VLLVP	LysM1
VTCGCAGNHSSANTS	113 aa
\mathbf{Y} QIQL \mathbf{GD} SYDFVATTLYENLTNWNIVQAS \mathbf{N} PGVNPYLLPERVK \mathbf{VVFP}	LysM2
LFCRCPSKNQLNKGIQYLIT	180 aa
YVWKPNDNVSLVSAKFGASPADILTENRYGQDFTAATNLPILIP	LysM3
VTQLPELTQPSSNGRKSSIHLL	246 aa
VILGITLGCTLLTAVLTGTLVYVYC	TM
RRKKALNRTASSAETADKL <u>LSGVSGYV</u> SKPNVYEIDEI T	KD
MEATKDFSDECKVGESVYKANIEGRVV <u>AVK</u> KIK <u>E</u> GGAN <u>EE</u> LKILQKV	
N <u>HGNLVKLMG</u> VSSGYDGNCFLVY E YAENGSLAEWLFSKSSGTPNS L T IV V	
WSQRISIAVDVAVGLQYMHEHTYPRIIHRDITTSNILLDSNFKAKIA VIa VIb	
${\tt NFA}$ MARTSTNPMMPKI ${\tt DVFAFG}$ VLLIELLTGRKAMTTKENGEVVMLWVII	
KDMWEIFDIEENREERIRKWMDPNLESFYHIDNALSLASLAVNCTAD	
KSLS <u>RP</u> SMAEIVLSLSFLTQQSSNPTLERSLTSSGLDVEDDAHIVTS XI	
ITAR	595 aa

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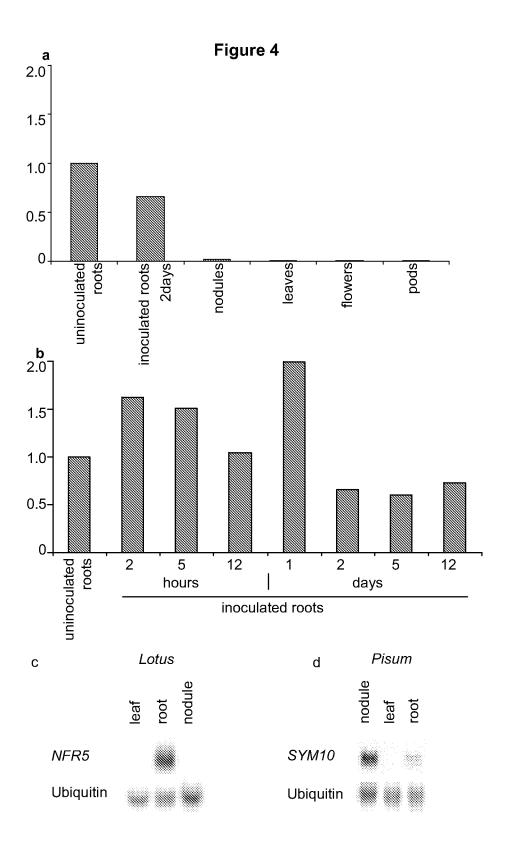
Figure 2

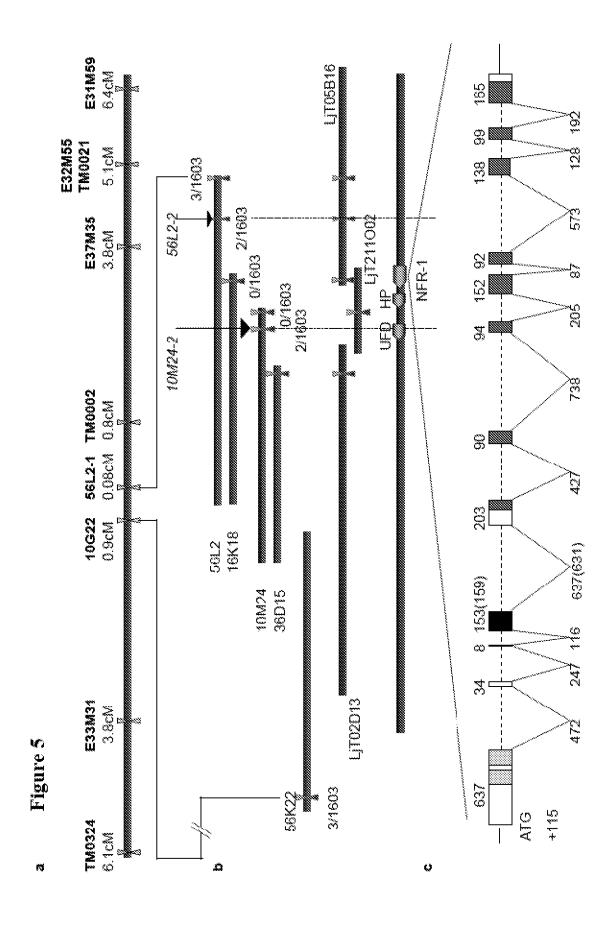
c

NFR5M1 SYM10M1 M.tM1 RiceM1	52:YTAQSPNLLSLTNISDIFDISPLSIARASNIDAGKDKLVPGQVLLVP:98 52:YFARSPNFLSLTNISDIFDMSPLSIAKASNIEDEDKKLVEGQVLLIP:98 53:YRAQSPNFLSLSNISDIFNLSPLRIAKASNIEAEDKKLIPDQLLLVP:99 47:YRTQSPGFLDLGNISDLFGVSRALIASANKLTTEDGVLLPGQPLLVP:93
NFR5M2 SYM10M2 M.tM2 RiceM2 VolvoxM2 Pfam	114: YQIQLGDSYDFVATTLYENLTNWNIYQASNPGVNPYLLPERVKVVFP:160 114: YTIKLGDNYFIVSTTSYQNLTNYVEMENFNPNLSPNLLPPEIKVVVP:160 115: YSIKQGDNFFILSITSYQNLTNYLEFKNFNPNLSPTLLPLDTKVSVP:161 109: YPIRPRDTFFGLAVTAFENLTDFYLVEELNPAAEATRLEPWQEVVVP:155 106: YTIQPGDTFWAIAQR.RGTTVDVIQSLNPGVNPARLQVGQVINVP:149 1: YTVKKGDTLWKIARR.YGISVSELKSLN.GLSSDNLYVGQKLKIP:43
NFR5M3 SYM10M3 M.tM3 RiceM3	181: YVWKPNDNVSLVSAKFGASPADILTENRYGQDFTAATNLPILIP: 224 181: YVWQANDNVTRVSSKFGASQVDMFTENNONFTASTNVPILIP: 222 182: YVWQDNDNVTLVSSKFGASQVEMLAENNHNFTASTNRSVLIP: 223 176: YVWQPGDDVSVVSALMNASAANIAASNGVAGNSTFATGQPVLIP: 219
d	VII VIII IX
Cons	<u>D</u> FG
Arab 50 NFR5 44 SYM10 44 M.t 45	5:KIADFGLSRDLYSDDYYKVKGGKLPIRWMAPESLKEGKFTSKSDVWSFG:248 0:KIANFGVARILDEGDLDLQLTRHVEGTQGYLAPEYVENGVITSKLDVFAFG:550 8:KIANFAMARTSTN PMMPKIDVFAFG:472 9:KIANFSMARTSTN SMMPKIDVFAFG:473 0:KIANFGMARTSTN SMMPKIDVFAFG:474 6:KLSNFSLAKPAAMVD AAATSSDVFAFG:502

Figure 3

SPLEIAKA: 79 SPLEIAKA: 79 SPLRIAKA: 80	PERVKVYF: 159 PPEIKVV: 159 PLDTKVSV: 160	. 240 Topssnar 239 Eopssnar 237 Eopssnar 239	BATKDPSD: 318 BATMULSB: 317 BGTTMLSD: 318	, 400 LF&KS>:398 LPSELSKT:396 LPSESSKT:397	, 480 V PAP GVLL:475 V PAP GV <u>V</u> L:476 V PAP GV <u>V</u> L:477	8RP <u>S</u> MARI:555 8RPSIARI:556 8RPTIARI:556	
. Leliniedipu Pleiniedipu Pleiniedipu	150 Menendervill Pr <u>uf</u> np <u>ills</u> ptil	230 JULIDALIOTE SVILIDALISTE	310 //SKPWYELDBIN //SKPTMYEMDAIN		470 ARTSTUDMARKID ARTSTU <u>S</u> MAPKID	550 . ASLAVNCTADKSI ASLAVNCTADKSI	
.50 Cetyvtytasseni Cetyvaypaseni Cetyvaypaseni	30 TTLYENLTWWNI TTSYONLTWYNEI ITSYONLTWYLEI	210 220 ENRYCODPTAATWI EN . WHETAETWI	290 300 WETADKILEGVEGT! WETADKILEGVEGT!	70 , , , 380 GVSSGYDGNCFI GVSSDHEGNCFI GVSS <u>DHI</u> GNCFI	50 de	530 , , , 540 ILESPYHIDNALSIL LENFYPIDNALSIL ILESFYPIDNALSIL	
. 10	TSVOLCOSYDEVATT PTYTICLGDNYFIVSTY TYSIKOGDNFFILSIT	70 180 190 200 210 220 230 240 280 240 240 280 240	290 KALNRTASSI KRLNRSTSLI	. 350 Ilokynhchlyklingy Ilokynhchlyklingy Ilokynhchlyklingy	410 470 490 788 DN SETWSORICIAVDVAVGLOYMHEHTYPRILHRDITTSNILLDSNFRARIANPAMARTSTNFMBFRIDVPAPGVIL: 475 SNSVVSETWSORITVAVDVAVGLOYMHEHTYPRILHRDITTSNILLDSNFRARIANPSMARTSTNEMPRIBVPAPGVVL: 475 SNSVVSETWSORITIAMDVAIGLOYMHEHTYPRILHRDITTSNILLGSNFRARIANPSMARTSTNEMPRIBVPAPGVVE: 477	. 520 Kerlikandphil Kerlikandpril Kerlikandpril	. 600 IGITAR:595 ISIVAR:594 ISVLAR:59
. , 30 , . TNIAARSEKISGI TNISAQPEGISGI TNISAQPEYISEI	CCECNESSANTS) CCTRNETEANT CCTRNESEANT	190 TYVWJANDRYSLVSA TYVWJDADRYILVSZI	, , , 270 TAVLESILVYVECKRI VVVLTISILVYVECIKRI	. 350	430 Loymhehtyprii Loymhehtyprii Loymhehtyprii	510 Emedraei poirenre Emederki polegnre Emederki polegnre	SCIDVEDIAHIVI CIDVER THVVI CIDARR THVVI
, , 20 LSLFLALT, LLF HALFLALM, FFV HALFLYCMLFFU	APGOVLLAFVTC REGOVLLIPVTC IPDOLLLEVY	190 Olekci <u>v</u> lity Olekciklity Olekciklity	260 . LGITLGCTLLTA IGISLGSAFFYY IGISLGSAFFIL	340 ANIEGROVAVK ANIEGROLAVKK ANIEGRO <u>L</u> AVKK	420 Cricanovavo Critanovaso	500 T <u>tkengrv</u> mem Timengrvy <u>i</u> em Ttkengrvy <u>i</u> em	Scephlersits Scephlersits Sc <u>e</u> phlersits
1. (4) 10 1. MAVEFITSSS 1. MATERIESSS	80; SNIDAGKDKLYDGOYLLYPYTCGCZGHESSANTSYDIOLGDSYDPYATTLYENLTWANIVOASNPGVNPYLLPERYKYYF; 159 80; SNIEDEDKKLYEGOYLLYPYTCGCZGHESSANTSYDIOLGDSYDPYATTLYENLTWANIVOASNPGVNPYLLPBEYKYYYF; 159 81; SNIEDEDKKLYEGOYLLYPYTCGCTKNHSFANITYSIKOGONNFFILSITSYONLTWYLERWHENPHLEPHLAPLDYKYSV; 150	160; PLRCRCPSKROLSKOIKUITTVOKPUBRYSLVSAKROASPADILTBURYGDPTAATULPILIPYTGIPELTGPSSKOR; 23 160; PLRCRCPSKROLSKOIKUITTVOKPUBRYSLVSAKROASPADILTBURYGDPTAATULPILIPYTGIPELTGPSSKOR; 23 161; PLRCRCPSKROLKKOIKUITTVVODNERYTLYSSKRGAS <u>OVEMLARKI, MHN</u> PTASTNRSVLIPYTSIPK <u>ILIQ</u> PSSKOR; 23	240, k. s<u>e</u>thelut 238, knstrkeafi 239, kss<u>sonea</u>li	350 370 380 380 340 350 400 350 350 350 350 370 370 380 380 380 380 380 380 380 380 380 38	410 470 480 480 480 480 480 480 480 480 480 48	476. IRLEFCREAMTTKRNGRYVNENKEDMEIPDIRENREREIRKWMDPNERSPYHIDNALSLANGCTADKSLSRPEMAEI.555 477:IRLEFCREAMTTKRNGRYVNENKEDMKIPDIRENREREIRKWMDPNERSPYHIDNALSLANGCTADKSLSRPEMAEI.555 478:IRLEFC <u>EKAMTTK</u> RNGRYVILMKD <u>PWEIPDLEGNRERELRKWMDPELRSPYD</u> IDNALSLASLANGCTADKSLSRPIJAEI.555	556.VLSLSFLTVQSSUPTLERSLTSSGLDVEDDAHIVESITAR;595 557.VLCLSLENQSSSEPMLERSLTSSGLDVEDDAHIVESITAR;595 557.VLCLSLENQSSSEPMLERSLTS.GLDVER.THVVTSIVAR;594 559.VLCLS <u>LEN</u> QDSS <u>EPM</u> LERSLTS.GLDARR. <u>THV</u> VTSVIAR;59
Lotus Pea M.t	Lotus Pea M.t	Lotus 1 Pes 1 M.t. 1	Lotua 2 Pea 2 M.t 2	Lotus 3 Des 3 M.t 3	Lotus 3 Pea 3 M.t 3	Lotus 4 Vea 4	Lotus 5 Pea M.t 5





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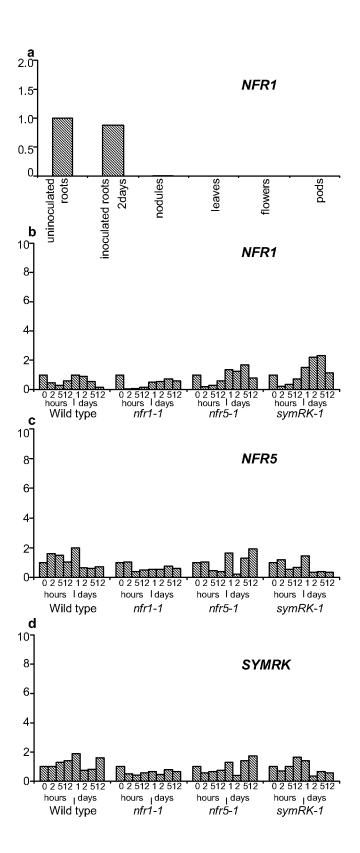
Figure 6a

MKLKTGLLLFFILLLGH	SP
VCFHVESNCLKGCDLALASYYILPGVFILQNITTFMQSEIVSSNDAITS YNKDKILNDINIQSFQRLNIPFP C D C IGGEFLGHVFE	103
YSASK <u>GD</u> TYET <u>IA</u> NLYYANLTTVDLLKRF <u>N</u> SYDPKNIPVNAKVNVT	LysM1
VN C S C GNSQVSKDYGLFIT	168
YPIRPGDTLQD <u>IA</u> NQSSLDAGLIQSFNPSV <u>N</u> FSKDSGIAF <u>IP</u>	LysM2
GRYKNGVYVPLYHR	224
TAGLASGAAVGISIAGTFVLLLLAFCMYV	TM
RYQKKEEEKAKLPTDISMALSTQD (GN) ASSSAEYETSGSSGPGTASAT GLTSIMVAKSMEFSYQELAKATNN	332 (324)
FSLDNKI gqgfgav yyaelrgkkt aik kmdvqast e flc e lkvlthv i ii iii	KD
HHLNLVR L IGYCVEGSLFLVY E HIDNGNLGQYLHGSGKEP LPW SS R VQ I A IV V VIa LDAAR G LE Y I H EHTVPVYI HRD V KS ANI LID KNLRGKVA DFG LTKLIEVG	
VIA VIB VII NSTLQTRLV G TF GY MP PE YAQYGDISPKI D VYAF G VVLFELISAKNAVLKT VIII * IX GELVAESKGLVALFEEALNKSDPCDALRKLVDPRLGENYPIDSVLKIAQLG	621 (623)
* RACTRDNPLLRPSMRSLVVALMTLSSLTEDCDDESSYESQTLINLLSVR* XI	

Figure 6b

SMART0257	YTVK <u>kg</u> DTlss <u>i</u> Arrygisvs <u>dl</u> Eln n il <u>dp</u> d n lqvgqklkip-
NFR1-M1	104-YSASKGDTYETIANLYYANLTTVDLLKRFNSYDPKNIPVNAKVNVT149
At21630-M1	105-YSVRQEDTYERVAISNYANLTTMESLQARNPFPATNIPLSATLNVLV-151
SMART 0257	YTVKKG D TLSSI A RRYGISVSDLLEL N N-ILDPDNLQVG1KLKI P
NFR1-M2	167-YPIRPGDTLQDIANQSSLDAGLIQSFNP-SVNFSKDSGIAFIP-208
At21630-M2	170-YPLRPEDSLSSIARSSGVSADILQRYNP-GVNFNSGNGIVYVP-211
BAB89226-M2	168-YAVQDGDTLGNIASLFRSSWKDILDLNPRVANPDFIKPGWILFIP-212
<i>Volvox</i> M	42-YTIQPGDTFWAIAQRRGTTVDVIQSLNP-GVNPARLQVGQVINVP-85

Figure 7



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Figure 8

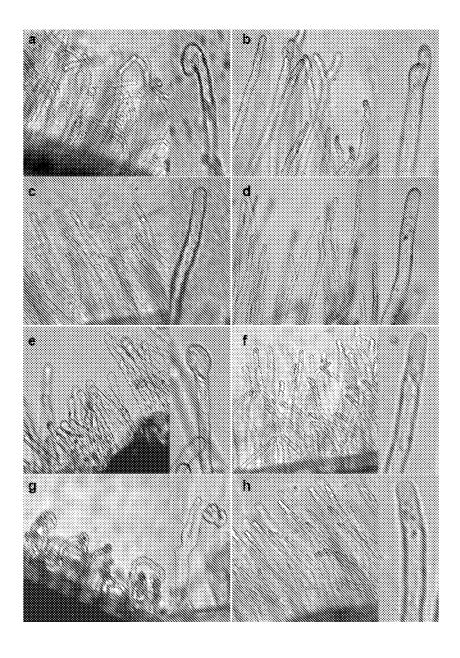
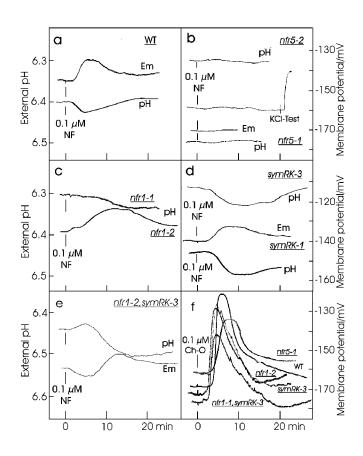


Figure 9



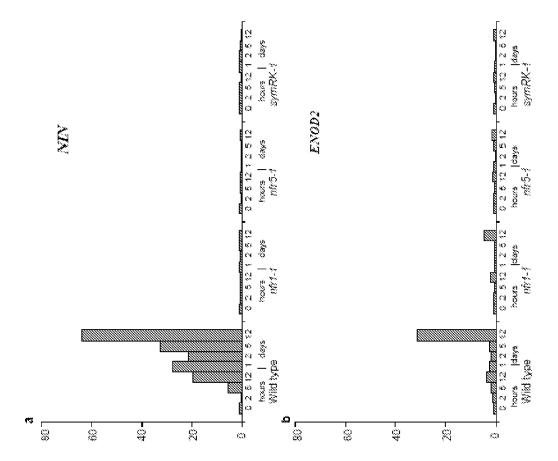


Figure 11

PGVFILGNITTFMQSEIVSSNDAITSYNKDKILNDINIQSFQRL	niaarbrisgpdfscpvdsppscrtvtvtzdspvllslinisdifdisplstapasnidask.drlvpg.gvl
BNCLKGCDLALASYVIL	SCPVDSPPSCETYVTYT
1:MKLKTG.ILLFFILLCHVCFHVESNCLKG	TSGSLSLFLALTLLFT
MFR1	MFRS

85 mipppciciggefichveesasegdtetianlytakletydlerpp. Sydpimipvnakvnvymcsechs, gvskdycletypirpgdtlodian 96 lupvicgcachessant, sygiclosydfvattlyeklenmnivgasmpsvmpylldbrvkvypplfcropsknolnksigyllitywkpmdnvslusa MFE1 NFE5 183:QSSLDAGLIGGFN. BSVNFSKDSGI.APIPGRYKNGVYVPLYHRTAGLASGAAVGISIAGTFVLLLLAFCMYVRYGKKBEEKAKIPTDISMALGTQDASS 195:KFGASPADILTENFYGQDFTAATNLPILIP.,,VT.,QLPELTQPS.,SNGRKS.,SIHLLVILGITLGCTLL.TAVLTGTLVYYCRRKKAIN,RTASS NFR1 NFR5

281, GABYETSSSSGPSTASATGLTSIMVAK SMEFSYGELAKATMMFSLDMK I GOGGFFSAVTVAELRGKKTAIKKMIVQASTBFLCELKVLTHVHBLMLVRLI G 283; ABTADKLLSG..., VSGY..., VSKPNVYBIDRIMBATKDFSDBCKVGES..., VYKANIEGRVVAVKKIKEGSANE... BLKILDKVNHGNEVKIMG MFR1 MFR5

381:YC..VEGSLPLVYEHIDMGMLSGYIHG.SGKEP..LFMSSRVQIALDAARGLEYIHEHTVPVYIHRDVKSANILIDRMLRSKVADPGLTKLIEVGNSTLQ 367;VSSCTICANCELVYEYAERGSLAEGIPSKSSCTPNSLIWSQRISIAVDVAVCLQYMBEHTTPRIIHRBITTSNILLDSTFKAKIANFAMAR.....TST.. NFR1 NFR5 476:TELVGTFGYMPPETAGYGDISPKIDVYAFGVVLFELISAKNAVL..KTGELVAESKGLVALFEBALNKSDFCDALRKLYDPRLGENYPIDSVLKIAQLGR 459:......NP.....NMPKIDVFAFGVLLIBILTGRKAMTTKENGBVVMLKKDMWEIPDIBENR...EERIRKMDPMLESFYHIDNALSLASLAV NFR1 NFR5

MFRI 574 a**ctronfelrdsmaslyvalmtisslte**dod**dssytes......**gtlinlesy**r** MFR5 540 a**ctronfslsrdsmaelylslitos**syterelessoldspanitysitar

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Figure 12

Protein domain structure of Lotus japonicus and Latus filicanits NFR1 and NFR5 proteins and of the hybrid proteins

